

Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile
65 70 75 80
Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg
85 90 95
Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro
100 105 110
Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu
115 120 125
Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr
130 135 140
Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys
145 150 155 160
Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val
165 170 175
Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr
180 185 190
Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly
195 200 205
Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr
210 215 220
Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg
225 230 235 240
Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly
245 250 255
Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp
260 265 270
Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu
275 280 285
Thr Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val
290 295 300
Pro Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr
305 310 315 320
Thr Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr
325 330 335
Thr Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr
340 345 350
Ser Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr
355 360 365
Gly Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr,
370 375 380

DI
sub
31-1

or wherein said derivative varies from said fragment only
by the substitution of 1 or 2 amino acids.

5. (Thrice amended) A composition according to claim 1 wherein the fragment or derivative includes part or all of the amino acid sequence consisting of amino acids 97-159 of the sequence shown in claim 1.

6. (Thrice amended) A composition according to claim 5 wherein the fragment or derivative includes a sequence having at least five amino acids identical with corresponding amino acids of a contiguous stretch of seven amino acids contained within amino acids 121-128 or 151-158 of the sequence shown in claim 1.

7. (Thrice amended) A composition according to claim 1 wherein the fragment or derivative includes a sequence having at least six amino acids identical with corresponding amino acids of a contiguous stretch of nine amino acids contained within amino acids 83-98 of the sequence shown in claim 1.

11. (Amended) A composition according to claim 1 wherein the fragment is of at least nine contiguous amino acids.

12. (Amended) A composition according to claim 11 wherein the fragment is of at least 13 contiguous amino acids.

- D4
13. (Thrice amended) A composition comprising a nucleic acid molecule which encodes a fragment or derivative as specified in claim 1.

14. (Twice amended) A composition according to claim 13 having part of the nucleic acid sequence shown below:

D5

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ccgctgggag tagctgcgac tcggcggagc cccggcggcg cgtccttggt ctaaccgggc 60
gcgcc atg acc gtc gcg cgg ccg agc gtg ccc gcg gcg ctg ccc ctc ctc 110
ggg gag ctg ccc cgg ctg ctg ctg gtg ctg ttg tgc ctg ccg gcc 158
gtg tgg ggt gac tgt ggc ctt ccc-cca gat gta cct aat gcc cag cca 206
gct ttg gaa ggc cgt acc agt ttt ccc gag gat act gta ata acg tac 254
aaa tgt gaa gaa agc ttt gtg aaa att cct ggc gag aag gac tca gtg 302
atc tgc ctt aag ggc agt caa tgg tca gat att gaa gag ttc tgc aat 350
cgt agc tgc gag gtg cca acc agg cta aat tct gca tcc ctc aaa cag 398
cct tat atc act cag aat tat ttt cca gtc ggt act gtt gtg gaa tat 446
gag tgc cgt cca ggt tac aga aga gaa cct tct cta tca cca aaa cta 494
act tgc ctt cag aat tta aaa tgg tcc acc gca gtc gaa ttt tgt aaa 542
aag aaa tca tgc cct aat ccg gga gaa ata cga aat ggt cag att gat 590
gta cca ggt ggc ata tta ttt ggc gca acc atc tcc ttc tca tgt aac 638
aca ggg tac aaa tta ttt ggc ccg act tct agt ttt tgt ctt att tca 686
ggc agc tct gtc cag tgg agt gac ccg ttg cca gag tgc aga gaa att 734
tat tgt cca gca cca cca caa att gac aat gga ata att caa ggg gaa 782
cgt gac cat tat gga tat aga cag tct gta acg tat gca tgt aat aaa 830
gga ttc acc atg att gga gag cac tct att tat tgt act gtg aat aat 878
gat gaa gga gag tgg agt ggc cca cca cct gaa tgc aga gga aaa tct 926
cta act tcc aag gtc cca cca acc gtt cag aaa cct acc acc acc aaa 974
gtt cca act acc gaa gtc tca cca aat tct cag aaa acc acc acc aaa 1022
acc acc acc cca aat gct caa gca acc ccg agt acc cct gtt tcc agg 1070
aca acc aag cat ttt cat gaa acc cca aat aaa gga agt gga acc 1118
act tca ggt act acc cgt ctt cta tct ggg cac acg tgt ttc acg ttg 1166

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aca ggt ttg ctt ggg acg cta gta acc atg ggc ttg ctg act tag 1211
 ccaaagaaga gttaagaaga aaatacacac aagtatacag actgttcccta gtttcttaga 1271
 cttatctgca tattggataa aataaatgca attgtgctct tcatttagga tgctttcatt 1331
 gtctttaaga tgtgttagga atgtcaacag agcaaggaga aaaaaggcag tcctggaatc 1391
 acattcttag cacacctaca cctcttgaaa atagaacaac ttgcagaatt gagagtgatt 1451
 cctttcctaa aagtgaaga aagcatagag atttgttcgt atttagaatg ggatcacgag 1511
 gaaaagagaa ggaaagtgat ttttccac aagatctgta atgttatttc cacttataaa 1571
 ggaaataaaa aatgaaaaac attatttga tatcaaaagc aaataaaaac ccaattcagt 1631
 ctcttctaag caaaattgct aaagagagat gaaccacatt ataaagtaat ctttggtctg 1691
 aaggcatttt catctttcct tcgggtggc aaaatatattt aaaggtaaaa catgctggtg 1751
 aaccaggggt gtgatggtg ataaggagg aatatagaat gaaagactga atcttccctt 1811
 gtgacacaaa tagagtgtg aaaaagcctg tgaaagggtg cttctttgac ttaatgtctt 1871
 taaaagtatc cagagatact acaatattaa cataagaaaa gattatatat tatttctgaa 1931
 tcgagatgct catagtcaaa tttgtaaatg ttattctttt gtaatatatta tttatatatta 1991
 tttatgacag tgaacattct gattttacat gtaaaacaag aaaagttgaa gaagatatgt 2051
 gaagaaaaat gtatttttcc taaatagaa taaatgatcc cattttttgg t 2102

or the nucleic acid sequence shown below:

tttaacggg cctctagac tcgagcggc gctgccatc ttgtcgtcgt cgtccttgta 60
 gtcgtgcatg tgggtggtggt ggtggtggtt aaccatggtg gcgggcccgc actgtgctgg 120
 atatctgcag aattcgatgg gcgtagctgc gactcggcgg agtcccggcg gcgcgtcctt 180
 gttctaaccg ggcgcgcc atg acc gtc ggc cgg cgg agc gtg ccc gcg gcg 231
 ctg ccc ctc ctc ggg gag ctg ccc cgg ctg ctg ctg ctg gtg ctg ttg 279
 tgc ctg ccg gcc gtg tgg ggt gac tgt ggc ctt ccc cca gat gta cct 327
 aat gcc cag cca gct ttg gaa ggc cgt aca agt ttt ccc gag gat act 375
 gta ata acg tac aaa tgt gaa gaa agc ttt gtg aaa att cct ggc gag 423
 aag gac tca gtg atc tgc ctt aag ggc agt caa tgg tca gat att gaa 471
 gag ttc tgc aat cgt agc tgc gag gtg cca aca agg cta aat tct gca 519
 tcc ctc aaa cag cct tat atc act cag aat tat ttt cca gtc ggt act 567
 gtt gtg gaa tat gag tgc cgt cca ggt taa aga aga gaa cct tct cta 615
 tca cca aaa cta act tgc ctt cag aat tta aaa tgg tcc aca gca gtc 663
 gaa ttt tgt aaa aag aaa tca tgc cct aat ccg gga gaa ata cga aat 711

ggt cag att gat gta cca ggt ggc ata tta ttt ggt gca acc atc tcc 759
 ttc tca tgt aac aca ggg tac aaa tta ttt ggc tcg act tct agt ttt 807
 tgt ctt att tca ggc agc tct gtc cag tgg agt gac ccg ttg cca gag 855
 tgc aga gaa att tat tgt cca gca cca cca caa att gac aat gga ata 903
 att caa ggg gaa cgt gac cat tat gga tat aga cag tct gta acg tat 951
 gca tgt aat aaa gga ttc acc atg att gga gag cac tct att tat tgt 999
 act gtg aat aat gat gaa gga gag tgg agt ggc cca cca cct gaa tgc 1047
 aga gga aaa tct cta act tcc aag gtc cca cca aca gtt cag aaa cct 1095
 acc aca gta aat gtt cca act aca gaa gtc tca cca act tct cag aaa 1143
 acc acc aca aaa acc acc aca cca aat gct caa gca aca cgg agt aca 1191
 cct gtt tcc agg aca acc aag cat ttt cat gaa aca acc cca aat aaa 1239
 gga agt gga acc act tca ggt act acc cgt ctt cta tct ggg cac acg 1287
 tgt ttc acg ttg aca ggt ttg ctt ggg acg cta gta acc atg ggc ttg 1335
 ctg act tag ccaaagaaga gttagaaga aaatacacac aagtatacag 1384
 actgttccta gtttcttaga cttatctgca tattggataa aataaatgca attgtgctct 1444
 tcatttagga tgctttcatt gtctttaga tgtgttagga atgtcaaca 1493

- D5
19. (Amended) A method of treating a patient having cancer, the method comprising administering to the patient a therapeutically effective amount of a composition as defined in claim 1.

- D6
34. (Amended) A composition according to claim 1, wherein said T cell epitope is a T cell epitope of said polypeptide of the CD55 family.

D7

Please cancel claims 2, 4, 8-10, 15-17, 20-24, 26-33, 35 and 36 without prejudice.